

|          |   |     |   |     |   |     |                  |        |    |
|----------|---|-----|---|-----|---|-----|------------------|--------|----|
| axmi008  | : | --- | VKKMSPYQNKNEYEILESSNN                           | --- | TNTPNRYPFANRDRMSTMSWDCQGISWDEIWES                   | --- | ---              | 80     |    |
| cry1Aa   | : | --- | ---   | --- | MDMNPINECIPYNCLSNPEVEVLG                            | --- | G--ERIETGYTPI    | 36     |    |
| cry1Ac   | : | --- | ---   | --- | MDMNPINECIPYNCLSNPEVEVLG                            | --- | G--ERIETGYTPI    | 36     |    |
| cry1Ia   | : | --- | MKLKNQDKHQFSSNAKVDKISTDS                        | --- | LKNETDIELQININHEDECLMSEYEN                          | --- | VEPFVSASTIQ      | 61     |    |
| cry2Aa   | : | --- | ---   | --- | MNVVNSGRITICDAYNVVAHDPFSFEHKS                       | --- | LDTIKEJMEWKRTDHS | 48     |    |
| cry3Aa1  | : | --- | MIRKGGKMNPNRSEHDTIKTITENNEVPTNHVQYPLAETPNPTLED  | --- | LNKYEFLRMTADNN                                      | --- | TEALDSTTKDVIQ    | 75     |    |
| cry3Ba   | : | --- | ---   | --- | MNPNNRSEHDTIKWTPNSELQTNHNQYPLADNPNSTLEELN           | --- | NYKEFLRMTEDESS   | 67     |    |
| cry4Aa   | : | --- | MNPYQNKNEYETLNASQKKLNISNMYTRYPIENSPKQLLQSTNYKD  | --- | WLNMCQONQ-QY--GGDFETFIDSGELS                        | --- | ---              | 71     |    |
| cry4Ba   | : | --- | ---   | --- | MNSGYPLANDLQGSMMKNTNYKDWLAMCENNQ-QY--GWNPAAINSS-SVS | --- | ---              | 46     |    |
| cry6Aa   | : | --- | ---   | --- | MIIDSKTTLPRHSLIHTIKLNSNKKYGPEDMTINGNQ               | --- | ---              | FIISKQ | 42 |
| cry7Aa   | : | --- | MNLNLDGVEDSNRTLN                                | --- | NSLNYPTQKALSPSLKMMNYQDFLSITEREQ                     | --- | PE--ALASGNTAIN   | 60     |    |
| cry8Aa   | : | --- | MSPNNQNEYEIIDATPSTSVSSDSNRYPFANEPTDAIQMMNYKDY   | --- | LKMSGGENPEL--FGNPETFISSSTIQ                         | --- | ---              | 70     |    |
| cry10Aa  | : | --- | MNPYQNKNEYEIFNAPSNGFSKSNMYSRYPLANKPNQPLKNTNYKDW | --- | LVNVCQDNQYQGNAGNFASSETIVGVS                         | --- | ---              | 74     |    |
| cry16Aa  | : | --- | MHYCGNRNEYDILNASSNDSNMSNTYPRYPLANPQDLMQNTNYKDW  | --- | LVNVCEGYHIEN--PR--EASVRAGLG                         | --- | ---              | 69     |    |
| cry19Ba  | : | --- | MNSYQNKNEYEILDAKRNTCHMSNCYPKYPLANDPQMYLRNTHYKDW | --- | WINMCEEASYAS  | --- | S--GPS           | 62     |    |
| cry24Aa  | : | --- | MNQYQNKNEYEILESSQNN                             | --- | MNMPNRYPFADDPNAVMMKNGNYKDWVNECEGSN                  | --- | ISPSAAA          | 60     |    |
| cry25Aa  | : | --- | MNPYQNKSECEILNAPLNN                             | --- | INMPNRYPFANDPNAVMMKNGNYKDWLNECDGITP                 | --- | SIFGTLG          | 60     |    |
| cry39Aa1 | : | --- | NSYENKNEYEILNDSKKS                              | --- | NMSNPYLRPYPLANDSLASMQNTNYKDWLTMCDRTDIDV--LS         | --- | SRGAVS           | 64     |    |
| cry40Aa1 | : | --- | NSYENKNEYEILESSNN                               | --- | TNMPNRYPFANDRDMSTMSFND                              | --- | CQGISWDEIWES     | 54     |    |

FIG. 1A

|          | * | 100                                       | *                                | 120                                | *            | 140 | *   | 160 |
|----------|---|---|----------------------------------|------------------------------------|--------------|-----|-----|-----|
| exmi008  | : | TITSIGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQ     | -TVS---                          | ALSIDLLSIIRKEVADSVLSDAIA           | -DFDGKLNRY   | :   | 133 |     |
| cry1a    | : | DISLSLTQFLLSEFVPGAGFVLGLVDIIUGIFCPSQ      | -----                            | WDAFPVQIEQLINORIEEFARNQAIS         | --RLEGLSNLY  | :   | 107 |     |
| cry1aC   | : | DISLSLTQFLLSEFVPGAGFVLGLVDIIUGIFCPSQ      | -----                            | WDAFLVQIEQLINORIEEFARNQAIS         | --RLEGLSNLY  | :   | 107 |     |
| cry1la   | : | TGIGIAGKILGTLGVPPFAGQVASLSYFILGELWP       | -KG-KNQ--                        | WEIFMEHVEEIIINQKISTVARNKALT        | --DLKGLGDAL  | :   | 135 |     |
| cry2a    | : | YVAPVVGTVSSFLKKVCSLIGKRILSELUGIIFPSG      | --STNLMQDILRETEQFLNORLNTDTLARVNA | --ELIGLOANI                        | :            | 124 |     |     |
| cry3Aa1  | : | KGISVVGDLGCVGFPFGGALVSFYTNFLNTIUPS        | ---EDP--                         | UKAFMEQVEALMDQKIADYAKNKALA         | --ELQGLQNNV  | :   | 148 |     |
| cry3Bb   | : | TGISVVGQILCVGVPFAGALTSFYQSFLNTIUPSD       | --ADP--                          | UKAFMAQVEVLIDKKIEEYAKSKALA         | --ELQGLQNNF  | :   | 141 |     |
| cry4Aa   | : | AVTIVVGTVLTCFGFTTPLGLALIGFGTLIPVLFPAQ     | -DQSNUTUSD                       | FITQTKNIKKELASTVISNANK             | --ILNRSFNVI  | :   | 148 |     |
| cry4Ba   | : | TALKVAGAILKFVNPPAGTVLTVLSAVLPILWPTNTP     | -TPERVUND                        | FWINTGNLIDQTVTAYVRTDANA            | --KMTVVVKDYL | :   | 123 |     |
| cry6Aa   | : | EWATIGAYIQTGLGLPVNEQQLRTHVNLSDISIPSD      | FSQLYDVVYCSDKTSAEWGNKNLYPLI      | IKSAND                             | -IASYGFVKVAG | :   | 121 |     |
| cry7Aa   | : | TVSVTGTATLSALGVPGASFITNFYVKIAGLLUPEN      | --GKI--                          | WDEFMTEVEALIDOKIEEYVRNKALIA        | --ELDGLGSAL  | :   | 134 |     |
| cry8Aa   | : | TGIGIVGRILGALGVPPFASQIASFYSFIVGQLWPSKS    | -VDI--                           | UGEIMERVEEELVDQKIEKYVKOKALA        | --ELKGLGNAL  | :   | 145 |     |
| cry10Aa  | : | AGIIVVGTMLGAFAPVLAAGIISFGTLLPIFUQGS       | DPAN---                          | VUQDLLNIGGRPIQIDKNIINVLTS          | --IVTPIKNQL  | :   | 149 |     |
| cry16Aa  | : | KGLGIVSTIVGFFGGSIIIDTIGLFYQISELLWPEDD     | -TQOYTUQD                        | IMNHVEDLIDKRITVIRGNAIR             | --TLADLQGV   | :   | 146 |     |
| cry19Ba  | : | QLFKVGGSIIVAKILG-MIPEVGPLLSUMVSLFUPTIE    | -EKNTVUED                        | MIKYVANLLKQELTNDTLNRATS            | --NLSGLNESL  | :   | 138 |     |
| cry24Aa  | : | ITSKIVSIWLKTLAKAVASSLADSIKSSLGISKTITENNVS | ---QVSMVQVHQI                    | INRRIQETILDIGES                    | -SLNGLVAIYN  | :   | 136 |     |
| cry25Aa  | : | VLASIVISTINLATSPSIGDAFALVSSIGEYWPETKT     | -----                            | SFPLSVADVNRILREALDQNAINRATG        | -KFNGLMDTYN  | :   | 134 |     |
| cry39Aa1 | : | TGVGMLSTILSLFGIPLIGEGIDLLGGAADFLWPES      | DGGHQYTUED                       | LMNHIEELMDERLETEKRTTALD            | --DLRGLKALL  | :   | 142 |     |
| cry40Aa1 | : | TITSIGIDLIEFLMEPSLGGINTLFSIIGKLIPTNHQ     | -SVS---                          | ALSIDLLSIIRKEVADSVLSDAICRFLDGKLNRY | :            | 130 |     |     |

FIG. 1B

|          | * | 180  | * | 200  | * | 220 | * | 240 |
|----------|---|--|---|--|---|-----|---|-----|
| exti008  | : | EYLSYLGAULKDGKPL-QKTNNSDIGQLVYFFKLSERDFNEILGGSLSRN----             | : | NAQVLLLPPTFAQAANVQLLLLRDAV                     | : | 208 |   |     |
| cry1a8   | : | QIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLLAQVQ-----            | : | NYQVPLLSVVYQAANLHLSVLRDVS                      | : | 176 |   |     |
| cry1aC   | : | QIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQ-----             | : | NYQVPLLSVVYQAANLHLSVLRDVS                      | : | 176 |   |     |
| cry11a   | : | AVYHDSLESUWGN-----RNNTRARSVVKSQYIAELMFVOKLPSFAVS-----              | : | GEEVPLLPPIYAQAANLHLLLRDAS                      | : | 204 |   |     |
| cry2a8   | : | REFNQQVDNFLMP-----TQNPVPLSITSSVNTMQQLFLNRLPQFIQIG-----             | : | YQLLLPLPFAQAANMHLSFIRDVI                       | : | 192 |   |     |
| cry3Aa1  | : | EDYVSALSSWQKNPV-----SSRNPHSQGRIRRELFSAESHFRNSMPSFAIS-----          | : | GVEVLFLLTVAQAANTHLFLLKDAQ                      | : | 220 |   |     |
| cry3Bb   | : | EDYVNALNSUKKTPL-----SLRSKRSDRIRRELFSAESHFRNSMPSFAVS-----           | : | KFEVLFLLTVAQAANTHLLLKDAQ                       | : | 213 |   |     |
| cry4Aa   | : | STYHNHLKTWEMNPN-----PQNTQDVRTQIQLVHYHFQNVIPELVNSCPPNPSPDCDYNNILVLS | : | SYAQAANLHLLTVLNQAV                             | : | 225 |   |     |
| cry4Bb   | : | DQYTTKFNWTKREP-----SYRTAVITQFNLTSAKLRETA                           | : | VYFSNLVGYELLLPIYAQVANFNLLLRDGL                 | : | 193 |   |     |
| cry6Aa   | : | DPSTKKDGYFKKLQD-----ELDNIVDNNSDDDAIAKAIKDFKARCG-----               | : | ILKEAKQYEEAAKNIVTSLDQF                         | : | 186 |   |     |
| cry7Aa   | : | DKYQKALADWLK-----QDDPEAILSVATEFRIIDSLFEFSMPSPFKVT-----             | : | GYEIPLLTVYAQAANLHLLLRDST                       | : | 203 |   |     |
| cry8Aa   | : | DVYQQSLEDWLEN-----RNDARTSVVSNQFIALDNFVSSIPSFASV-----               | : | CHEVLLLA                                       | : | 214 |   |     |
| cry10Aa  | : | DKYQEFFDKWEPAR-----THAMAKAVHDLFTTLEPIIDKDLMLKNN-----               | : | ASYRIPTLPAYAQAIA                               | : | 218 |   |     |
| cry16Aa  | : | DDYNNWLKKWKDDP-----KSTGNLSTLVTKFTALDSDFNGAIRTVNNQGS--              | : | PGYELLLLPVYAQIANLHLLLRDAQ                      | : | 218 |   |     |
| cry19Bb  | : | NIYNRALAAWKQNK-----NNFASGELIRSYINDLHILFTRDIQSDFSLG-----            | : | GYETVLLPSYASAAANLHLLLRDVA                      | : | 208 |   |     |
| cry24Aa  | : | RDYLGALAEAWNKK-----SNINYQTNVAAEFKTVEREFFTKLKGIVRTS-----            | : | SSQITLLPFTTQAANLHLSMLRDAV                      | : | 206 |   |     |
| cry25Aa  | : | TVYLNQDWDYDTRIPANPQGSQIREAARRSLEEFIERDFRKALAGEFAEAG-----           | : | SQIVLLPIYAQAANTHLILKDAW                        | : | 210 |   |     |
| cry39Aa1 | : | GLFRDAFDSUEKNQ-----NDPIAKNRVGGYFEDVHTFVKDMASIFSAT-----             | : | NVEVLLLPVYAQAANLHLLLRDGV                       | : | 212 |   |     |
| cry40Aa1 | : | EYLLPYLEAULKDGKPL-QKTNNSDIGQLVKYFELS                               | : | ERDFNEILGGSLSARN-----NAQILLLPVFCASCCKQLLLLRDAV | : | 205 |   |     |

FIG. 1C

|         | * | 260   | *   | 280  | *   | 300                                  | *   | 320         |
|---------|---|---|-----|--|-----|--------------------------------------|-----|-------------|
| axmi008 | : | QYKAQWFFLSAENVRSELISPNSGCDFTGDYERLCKCTAEYTNVCLYUQVGLNQIKQGGTGADT  | --- | USKFNKFR   | :   | 284                                  |     |             |
| cry1a   | : | VFGQRWGFDA  | --- | TINSRYNDLTRLIGNYDYAVRWYNTGLERWGPDSRD                     | --- | WVRYNQFR                             | :   | 234         |
| cry1a   | : | VFGQRWGFDA  | --- | TINSRYNDLTRLIGNYDYAVRWYNTGLERWGPDSRD                     | --- | WVRYNQFR                             | :   | 234         |
| cry1a   | : | IFGKEWGLSS  | --- | EISTFYNRQVERAGDYSCHVCVKWYSTGLNNLRGTMAES                  | --- | WVRYNQFR                             | :   | 262         |
| cry2a   | : | LNADWGISAT  | --- | LRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEFR                | --- | TYMFLNVFEY                           | :   | 255         |
| cry3a   | : | IYGEWGYEKE  | --- | DIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSYES                     | --- | WVNFNRVRR                            | :   | 278         |
| cry3b   | : | VFGEWGYSE   | --- | DVAEFYHRQLKLTQYTDHCVNWNVGLNGLRGSTYDA                     | --- | WVKFNRFR                             | :   | 271         |
| cry4a   | : | KFEAYLKNNRQFDYL   | --- | EPLPTAIDYYPVLTKAIEDYTNVCTTYKKGLNLIKITTPDSNLDGMLNNTYNTYRT | --- |                                      | :   | 297         |
| cry4b   | : | INAEWGLAR   | --- | S  | --- | AGDQLYNTMVQYTKYIAHSITWYNKGLDVLRNKSNG | --- | Q-WITFNDYKR |
| cry6a   | : | LHGDQKKLEGVIN   | --- | IQKRLKEVQTAALNQAHGESSPAHKELEKVKNLKT                      | --- | TIER                                 | :   | 238         |
| cry7a   | : | LYGDKWGFTQN   | --- | NIEENYNRQKKRISEYSDHCTKWYNSGLSRLNGSTYEQ                   | --- | WINYNRFR                             | :   | 261         |
| cry8a   | : | IFGEWGFPG   | --- | EISRFYNRQVQLTAEYSDYCVKWKYKIGLDKLGTTSKS                   | --- | WLNHYHQFR                            | :   | 272         |
| cry10a  | : | TYYNLWLNQNGINPSTFN  | --- | SSNYQGYLKRKIQEYTDYCIQTYNAGLTMIRTNAT                      | --- | WNNYNTYRL                            | :   | 283         |
| cry16a  | : | IYGDKWSARANA  | --- | RDNYQIQLEKTEYIEYCINWYNKGLNDFRTAGQ                        | --- | WVNFNRVRR                            | :   | 275         |
| cry19a  | : | IYG-KELGYPST  | --- | VEFYNEQKYYTEKYSNYCVNTYKSGLESKKQIG                        | --- | USD FNRVRR                           | :   | 263         |
| cry24a  | : | MYQEGONLQSHIN   | --- | YSKELDDALEDYTNVCEVYTKGLNALRGSTAD                         | --- | WLEFNSFR                             | :   | 262         |
| cry25a  | : | QFRDGLGLIRPVC   | --- | VPITTSADPFSEFLRIMKYTDHCISYYDDGLAKIRSGSDG                 | --- | ETUWEFNKFR                           | :   | 278         |
| cry39a  | : | IYGSRWGIAPA   | --- | ADFYHDQLLKTYAIYANHCVTGYNNGLAQKELFAKSPN                   | --- | WNRFNAYRR                            | :   | 271         |
| cry40a  | : | QYEEQWFFLSAENVRSELISPNSGCDFTGDYERLCKCTAEYTDYCEYUQVAGLNQIKQAGTGADT | --- | WAKFNKFR   | :   | 281                                  |     |             |

FIG. 1D

|          |   |  |   |     |
|----------|---|--|---|-----|
| exmi008  | : | EMTLAVLDIIAIFPTYDFEKYPLP-----THVELTREIYTDVGYSSGTYSWLRNUPNTFNGLEAN-----GTRGPGL  | : | 352 |
| cry1a    | : | ELTLTVLDIVALFSNYDSRRYPPIR-----TVSQLTREIYTNPVLENFDGSGFRGMAQRIEQN-----IRQPHL     | : | 296 |
| cry1a    | : | ELTLTVLDIVALFPNYDSRRYPPIR-----TVSQLTREIYTNPVLENFDGSGFRGSAQGIERS-----IRSPHL     | : | 296 |
| cry1a    | : | DMTLMVLDLVALFPYSYDTOMYPIK-----TTAQLTREVYTDAGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHL  | : | 335 |
| cry2Aa   | : | VSIQSLFKYQSLMVSSGANLYASG---SGPQQTQSFTAQNPFLYSLFQVNSNYILSGISGTRLS-----ITFPNI    | : | 323 |
| cry3Aa1  | : | EMTLTVLDLIIALFPLYDVRLYPKE-----VKTELTRDVLTDPIVGVNLRGCGTTFNSNIEN-----YIRKPHL     | : | 341 |
| cry3Bb   | : | EMTLTVLDLIIALFPFYDIRLYSKG-----VKTELTRDIFDPIFSLNTLQEGPTFLSIEN-----SIRKPHL       | : | 334 |
| cry4Aa   | : | KMTTAVLDLVALFPNYDVCKYPIC-----WQSELTREIYQVLNFEESPYKYDYFQYQEDSLT-----R-RPHL      | : | 359 |
| cry4Bb   | : | EMTIQVLDIILALFASYDPRRYPADKIDNTKLSKTEFREIYTALESPTS--SK-SIAALEAALT-----R-DVHL    | : | 317 |
| cry6Aa   | : | -T-IKAEQDLEKKVEYSFLLGPLLG-----FWVVEILENTAVQHIKNQIDEIKKQLDSAQHDLD-----RDVKI     | : | 300 |
| cry7Aa   | : | EMILMALDIIAVFPFHDPRRYSME-----TSTQLTREVYTDPVSLISINPDIGPSFSQMEN-----TAIRTPHL     | : | 325 |
| cry8Aa   | : | EMTLVLDLVALFPNYDTHMYPIE-----TTAQLTRDVYTDPIAFNIYVSTGFCNPWSTHSGILFYEVENNVIRPPHL  | : | 345 |
| cry10Aa  | : | EMTLTVLDLIIAIFPNYDPEKYPIG-----VKSELIREVYTNVNSDTFR-----TITILENG-----LTRNPTL     | : | 341 |
| cry16Aa  | : | EMTLTVLDIISMFPIYDARLYP-----TEWKTELTREIYSDVINGEITYGLMTPYFSFEKAES-----LYTRAPHL   | : | 340 |
| cry19Bb  | : | EMTLSVLDIVALFPLYDTGLYPSK--DGKIHVKAELTREIYSDVINHDVYGLMVPYISFEHAES-----LYTRRPHA  | : | 333 |
| cry24Aa  | : | DMTLMVLDLVAIFPNYNPVRYPPLS-----TKISLSRKIYTDVGRDTDSPSGDWTNTGRTLAN-FNDLEREVTDSPSL | : | 334 |
| cry25Aa  | : | EMTLTVLDLVALYPYTHNIKLYPIR-----TQTELSRWVYTDVGCFCGNRKSDIFSRNLFDYLEN-----RLTRPREP | : | 345 |
| cry39Aa1 | : | DMTITVLDIILALFPTYDARLYTKP-----IKTELTREIYSDVLNLDVYGVQQTDLNKNAAAF-----TRSPHL     | : | 334 |
| cry40Aa1 | : | EMTLTVLDIILAIQTDFEKYPLP-----THVELTREIYTDVGYSSGTYSWLKYYTGAFTNLEAN-----GTRGPGL   | : | 349 |

FIG. 1E

|          |   |   |   |     |
|----------|---|---|---|-----|
| exti008  | : | VTULSKIGIYNEYVSR-----YFAGVGTGRHYEDYTKGN-----GIFORMSGTTSNDLRNIDFQADVYKITS LAIM         | : | 419 |
| cry1Aa   | : | MDILNSITIYDVRHG-----FNYUSGHQITASPVGFSGP-EFAPPLFGNAGNAA-PP-VLVS LTGLGIFRTLSSPL         | : | 365 |
| cry1Ac   | : | MDILNSITIYDAHRG-----YYWUSGHQIMASPVGFSGP-EFTFFPLYGTMGNAA-PQQRIVAQLGQGVYRTLSSTL         | : | 366 |
| cry1Ia   | : | LDLEQVTIYSLLS---RWSNTQYMMWGCHKLEFRTIGGTLN-ISTQGSTNTSINPV-TLPFTSRDVYRTESLAGLNL         | : | 410 |
| cry2Aa   | : | GGLPGSTTTHSLNSARVNYSGVSSGLIGATNLNHNFCSTVLPPLSTPFVRSWLDSCIDREGVATSTNQOTESFQTLS         | : | 403 |
| cry3Aa1  | : | FDYLHRIQFHRFQP---GYVENDSFNYWUSGNYVSTRPSIGSND-IITSPFYGNKSSSE---PVQNL EFNKEKVYRAVANLNL  | : | 416 |
| cry3Bb   | : | FDYLGQIEFHRLOP---GYFEKDSFNYWUSGNYVEIRPSIGSSK-TITSPFYGDKSTE---PVQKLSFDGQKVYRTIANIDV    | : | 409 |
| cry4Aa   | : | FTWLDLSLNFYEKAQTT---P-----NNFFTSHYMMFHYTLDNIS-QKSSVFG-NHNVID-KLKSGLGATNIYIFLLNVISL    | : | 429 |
| cry4Ba   | : | FTWLKRVDFTWNTIYQ---D-----LRFLSANKIGFSYINSSAM-QESGIYGS SGFGSN-LTHQIQLNSNWKTSITDTSS     | : | 388 |
| cry6Aa   | : | IGMLNSINTDIDNLYSQGQEAIKVFQKLGQIWA TIGAQIENLR-TTSLQEVQDSDDADEIQIELEDA SDAMLVVAQEARD    | : | 379 |
| cry7Aa   | : | VDYLD ELYIYTSKYKAFSHEIQPDLFYWSAHKVSFKKSEQSN--LYTTGIYGKTSGYI-SSGAYSFHGNDIYRTLAAPSV     | : | 402 |
| cry8Aa   | : | FDILSSVEINTSRGCI-TLNNDAYINWUSGHTLKYRRTADSTV-TYTANYGRITSEKN-SFALED RDI FEINSTVANLAN    | : | 422 |
| cry10Aa  | : | FTWINQGRFYTRNS-----RDILD PYDIFSFTGNQMA-FTHINDDRNIIUGAVHGMIIISQDTSKVFFPYRNKPI          | : | 409 |
| cry16Aa  | : | FTWLKGRFRVWNSISY-----WTFLSGGQNKYSYTNNS-S-INEGSFRGQD TDYGGTSSSTINIPSN SYVYNLWTE NY     | : | 410 |
| cry19Ba  | : | FTWLKGRFRVWNSINS-----WTFLSGGENRYFLTHGEGT-IYNGPFLGQDTEYGGTSSYIDISNNSS IYNLWTKNY        | : | 404 |
| cry24Aa  | : | VKWLGDMTIYTG AIDSYRPTSPGDRIGVWYGNINAFYHTGRID-VVMFRQTGDTAYEDPSTFISN ILYDDIYKLDLRAAA    | : | 413 |
| cry25Aa  | : | FNYLNSVQLFASTVSN---SNN---GEVLRGNLKMIMFEGGJTA-SRSGDGVITGTTPFSTMDWSYGGYPRKHVAFITSR      | : | 419 |
| cry39Aa1 | : | VTRLRGFD FYTRTKYA-----Y---WRYLAGHTN YFSFTENG-----TIYSSSFNNWYDIDMTKSTINIPDYANIYKLWTKSY | : | 404 |
| cry40Aa1 | : | VTWLRSIGIYNEYVSR-----YFSGVGTGRHYEDYTTGN-----GNFORMSGTTSNDLRD ISFPNSDIFKIESKAIM        | : | 416 |

FIG. 1F

|          |   |  |     |   |     |   |     |   |                     |
|----------|---|--|-----|---|-----|---|-----|---|---------------------|
| exmi008  | : | N---   | 500 | * | 520 | * | 540 | * | 560                 |
| cry1a8   | : | LVGETTARPEYRVSKADFRVWGGPDLNVDAGNGLSRMTIESTFPLVLHSHN          |     |   |     |   |     |   | CVRCPSHRLSNAACVVY   |
| cry1aC   | : | YRRILG-SGPNQELFVLDGTEFASFALTNL PSTIYRQGTVDSLDVIPPQDMS        |     |   |     |   |     |   | VPFRAGFSHRLSHVTMLSQ |
| cry1la   | : | YRRPFN--IGINNQLSVLDGTEFAYG-TSSNLPAAVYRKSGTVDSLDEIPPQNNN      |     |   |     |   |     |   | VPFRQGFHRLSHWSMFRS  |
| cry2Aa   | : | LTQPVNGVPRVDFHUKFVTHPIASDNFFYPFGYAGIG----                    |     |   |     |   |     |   | QPMVESYSHRLSHIGLISA |
| cry3Aa1  | : | LRCGAFSARGNSNYFPDYFIRNISCVPVIRMEDLTRPLHYNQIRNIESPSGTPGG      |     |   |     |   |     |   | ARAYLVSVHNRKNNIY    |
| cry3Bb   | : | AVWPS-AVYSGVTKVEFSQYNDQIDEASTQYDSKRN-VGAVSUDSIDQLPETID       |     |   |     |   |     |   | EPLEKGYSHQLNYYVMCFM |
| cry4Aa   | : | AAAPNGKAVYLCVTKVDFSQYDDQKNETSTQYDSKRNHGVSAQDSIDQLPETID       |     |   |     |   |     |   | EPLEKAYSHQLNVAECFLM |
| cry4Ba   | : | DNKYLNDYNNISKMDFFITNGTRLLEKELTAGSGQITVDVKNIFGLPILKRRENQGNPTL |     |   |     |   |     |   | FPTVDNYSHILSFIKSLSI |
| cry6Aa   | : | P---S---NRVTKMD FYKIDGTLASYNSTPTP---                         |     |   |     |   |     |   | PTVNDYTHILSVIKTDWI  |
| cry7Aa   | : | FTLMAYSTNSRQNL PINVISDSMCSTINMTSNQYSNPTINMTSNQYMSHEYTSLP     |     |   |     |   |     |   | NNFMLSRMSNLEYKC     |
| cry8Aa   | : | WVYPY---TONYGVQEVEFYGVKGVHVRGDNKYDLT-----                    |     |   |     |   |     |   | YDSIDQLPPDGE        |
| cry10Aa  | : | YYQKAYGVPGSWFHMVKGRTSSTTAYLYSKITHALQG--CTQVYESSEIPLDRT       |     |   |     |   |     |   | PIHEKYTHRLCHATAIFK  |
| cry16Aa  | : | DKVEIVRHREYSDI IYEMIFFSNSSEVFRYSSNSTIENNYKRTDSYMPIKQTKNE     |     |   |     |   |     |   | VPVAESYSHRLSHITSHSF |
| cry19Ba  | : | EYIYPUGDPWNITKNNPFSVIDNNSSEKELIYGHRINPKPVWRTDFDLTNKEGTEL     |     |   |     |   |     |   | EYGHTLSYIKTDNY      |
| cry24Aa  | : | EWIYPWIDPWNITKINFSITDNSNSESIYCAERMNKPTVWRTDFNFLNMRAGNCP      |     |   |     |   |     |   | AKVNDYNHILSYMLINGE  |
| cry25Aa  | : | VSTIQGANDTTFGVSSSRFFDIRGNQLYQSNKFPYPSLPITITTFPGEESSEGNAN     |     |   |     |   |     |   | TTYNDYNHILSYMLINGE  |
| cry39Aa1 | : | QALPGLNNSIHVIVIGIDSFRAICPGCGQGDHTFSLPGGDMYDCGKVQINPLEDYRNS   |     |   |     |   |     |   | DYSHLLCDVKILQE      |
| cry40Aa1 | : | TNISPYTD PVGISQMOPSLTNQQLTYIGTSAPKYP-----                    |     |   |     |   |     |   | DHWISDMNTINQSVQL    |
|          | : | N---   |     |   |     |   |     |   | LTVENYSHILSYMTSAQH  |
|          | : |  |     |   |     |   |     |   | SYRDYSHRLSNAACVGA   |

|          | * | 580  | * | 600 | * | 620 | * | 640 |
|----------|---|--|---|-----|---|-----|---|-----|
| axmi008  | : | GNS-----RVNVYGWHTSLKRENIIEANQITQIPAVKSYYLQNYLANAYTV--IKGHTTGGDLIRFLRTKSEYNNAVY :     |   |     |   |     |   | 560 |
| cry1a    | : | AAG--AWYTLRAPTFSSUQRSAEFNNIIPSSQITQIPTLKSTNLGSGTSV----VKGPGFTGGEDILRRTSPG----- :     |   |     |   |     |   | 505 |
| cry1Ac   | : | GFSNSSVSIIRAPMFSSUIHRSAEFNIIIASDSITQIPAVKGNFLFNGSVI-----S-GPGFTGGDLVRNLSSEN---NIQ :  |   |     |   |     |   | 509 |
| cry1ie   | : | S-----HVKAIVYSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAUV----VRGPGFTGGEDILRRTN-----T :         |   |     |   |     |   | 541 |
| cry2Aa   | : | AAN-----ENGTMIHLPEDYTGTFTISPIHATQVNQNTRTFISEKFGN-----Q-----GDSLRFEQSN----- :         |   |     |   |     |   | 529 |
| cry3Aal  | : | QGS-----RGTIPLVTWTHKSVDFFNMIDSKKITQLPLVKAYKLQSGASV----VAGPRFTGGEDIIOCTE-----M :      |   |     |   |     |   | 551 |
| cry3Bb   | : | QDR-----RGTIPTFTWTHRSVDFENTIDAEEKITQLPVVKAYALSSGASI-----IEGPGFTGGENLLFLKESS-----N :  |   |     |   |     |   | 548 |
| cry4Aa   | : | PATY-----KTQVYTFATWTHSSVDPKNTIYTHLTITQIPAVKANSLGTASKV----VQGPCHTGCDLIDFKDHFK---IT- : |   |     |   |     |   | 576 |
| cry4Ba   | : | DYN-----SNRVSFAWTHKIIVDPNNQIYTDALTQVPAAKSNFLNATAKV----IKGPGCHTGCDLVALTSNGT---LSG :   |   |     |   |     |   | 519 |
| cry6Aa   | : | P-----ENNFMIVGVNNSDUWNNSDUWYNN----- :  |   |     |   |     |   | 475 |
| cry7Aa   | : | STP--DYDNATIPIFSWTHRSAEYYNRRIYPNKITKIPAVKNYKLDPPSTV----VKGPGFTGGEDLVKRGS-----T :     |   |     |   |     |   | 531 |
| cry8Aa   | : | SKNG-SAYYGSPFPVFWHTSTSADLNNTIYSDKITQIPAVKGDMLYLGGSV----VQGPFTGGEDILKRIN-----P :      |   |     |   |     |   | 560 |
| cry10Aa  | : | IFSVMR--ERRRVAFSWHTSVDFQNTIDLNTITQIHAKALKVSSDSKIVK-----GPGHTGGEDLVILKDSMD----- :     |   |     |   |     |   | 546 |
| cry16Aa  | : | TFGQ----KRHCYSFATHSSVDPMMNTIAANKITQIPVVVKASSINGSISI----EKGPGFTGGEDLVKMRAVS----- :    |   |     |   |     |   | 547 |
| cry19Ba  | : | TFGQ----KRHCYSFATHSSVDRYNTIVPDKIVQIPAVKTNLVGANILK-----GPGHTGGEDLLKLEYER----- :       |   |     |   |     |   | 539 |
| cry24Aa  | : | DSSNICEGRSSLSHAETHASLDRNNTILPDEITQIPAVTAAYELRGNSS-----VVACPESTGGEDLVKMSYHS----- :    |   |     |   |     |   | 550 |
| cry25Aa  | : | ASNPTQTFAFSALSGLWHSSAGNRNVVYVDKITQIPATKTIVREHPMIK-----GPGFTGGEDLADLSSNS---DIL :      |   |     |   |     |   | 559 |
| cry39Aal | : | FGD-----KKIGYTFAWMHESVDFDNRVDPDKITQIPAVKGDYLQGYVK-----QGPGHTGGEDLVSMIRTDR----- :     |   |     |   |     |   | 536 |
| cry40Aal | : | GNS-----RINVYGWHTSMSKYNLIIYDPDKITQIPAVKAFDISDTGP--GQVI-ACPGHTGCNVVWSLP-----YY :      |   |     |   |     |   | 548 |

**FIG. 1H**



|          | * | 660  | *                 | 680                 | *                 | 700 | *   | 720 |  |
|----------|---|--|-------------------|---------------------|-------------------|-----|-----|-----|--|
| exmi008  | : | AGGGIRLIINMKTAGQSYRIRIRFRYAADKAFFSVLYPGGUGSNRFVSLKSYSGNY                           | ----              | DDLKYSDFKFAELIITPP  | :                 | 634 |     |     |  |
| cry1Aa   | : | -QISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDG--RPINQGNFSATSSG                             | -----             | SNLQSGSFRVTGFTTFF   | :                 | 574 |     |     |  |
| cry1Ac   | : | MRGYIEVPIHFPTSTIRYRVRIRYASVTPIHLNVNUGN--SSIFSNTVPATATSL                            | -----             | DNLQSSDFGYFESANAF   | :                 | 579 |     |     |  |
| cry1Ia   | : | GTFGDIRVNIINPPFAQRYRVRIRYASTTDLQFHTSING--KAINQGNFSATMNRG                           | -----             | EDLDYKTFRTVGFITPP   | :                 | 611 |     |     |  |
| cry2Aa   | : | -----TTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTINNDGVN                          | -----             | DNGARFSDINIGNIVASD  | :                 | 599 |     |     |  |
| cry3Aa1  | : | GSAATYVTPDVSYSQYRARIHYASTSQITFTLSLDG--APFNQYYFDKTIKNG                              | -----             | DTLTYSNFWNLASFSTPP  | :                 | 621 |     |     |  |
| cry3Bb   | : | SIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSN--NDFVIYINKIMNKD                             | -----             | DDLTQTFDLATINSNM    | :                 | 618 |     |     |  |
| cry4Aa   | : | -----COHSNFOQSYFIRIRYASNG--SANTRAVI--NLSIPGVAELGMALNPFTSGTDYTNLKYKDFQYLEFSNEV      | -----             |                     | :                 | 644 |     |     |  |
| cry4Ba   | : | RMEIQCKTISIFNDPTRSYGLRIRYAANSPIVLNVSYVL--QGVSRGTTISTESTFSRPNNIIPITDLKYEEFRYKDPFDAI | -----             |                     | :                 | 597 |     |     |  |
| cry6Aa   | : | -----  | -----             |                     | :                 | -   |     |     |  |
| cry7Aa   | : | GYIGDIKATVNSPLSQRYRVRIRYATNVSGQFNVIYIND--KITLQTKFQNTVETIGEG                        | -----             | KDLTYGSGFGYIEYSTTI  | :                 | 604 |     |     |  |
| cry8Aa   | : | SILGTFAVTVNGSLSQRYRVRIRYASTTDFEFTLYLG--DTIEKNRFNKTMDNG                             | -----             | ASLTVETFKFASFITDF   | :                 | 629 |     |     |  |
| cry10Aa  | : | -----FRVRFLKNVSRQYQVRIRYATNAPKTTVFLTGIDTISVELPSTTSRQNP                             | -----             | ATDLTYADFGYVTFPRTV  | :                 | 614 |     |     |  |
| cry16Aa  | : | ---GLTMRFKAELLDKKYRVRIRYKCNYSKLLLRKWKGEYIQQIHNIPTSYG                               | -----             | AFSYLESFTITTTENIF   | :                 | 616 |     |     |  |
| cry19Ba  | : | ---FLSLRIK-LIASMTFRIRIRYASNISGQMMINIG----  | YQNPTYFNIIPTTSRDY | -----               | TELKFEDFQLVDTSYIY | :   | 606 |     |  |
| cry24Aa  | : | -----VWSFKVVCSELKNYRVRIRYASHGNCQFLMKRWPSTGVAPRQWARHNVQGTFS                         | -----             | NSMRVEAFKYLDIFTIT   | :                 | 620 |     |     |  |
| cry25Aa  | : | QYDLRSYDDRLTEDVPFRIRIRIRYASIGVSTISVDNUG--SSSPQVIVASTAAS                            | -----             | LDTLKYESFQYVVSIPENY | :                 | 629 |     |     |  |
| cry39Aa1 | : | -----LGINVYFPQPLDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVDGQPT                            | -----             | FDPMDFSAFRVVEVPASF  | :                 | 604 |     |     |  |
| cry40Aa1 | : | SRLKIRLIP--ASTNKNYLVRVRVYTSNGHLLVERUSPSSIINSYFFFLPSTGPG                            | -----             | DSFGYVDTLVITTFNQP-  | :                 | 617 |     |     |  |

FIG. 11

|          | * | 740  | *  | 760              | * | 780 |
|----------|---|--|--|------------------|---|-----|
| axmi008  | : | LPSSN---   | IQMDVEMQANSFQSDVNVVLDKIEFLPSNTTILEYEGERDLEKTKNAVNDLFTN | :                |   | 693 |
| cry1Aa   | : | NFSNG----  | SSVFTLSAHVFNCSGNEVYIDRIEFVPAEVTFEAE---                 | YDLERAQKAVNELFTS | : | 629 |
| cry1Ac   | : | TSSLG----  | N---IVGVRNFGTAGVIDRFEFIPVTATLEAE---                    | YNLERAQKAVNALFTS | : | 631 |
| cry1Ia   | : | SFLDV----  | QSTFTTIGAWNFSNGNEVYIDRIEFVFPVEVTYEAE---                | YDFEKAQEKWTALFTS | : | 666 |
| cry2Aa   | : | WINVT-----   | LDINVTLSGTPFDLMNIMFVPTNLPPLY-----                      |                  | : | 633 |
| cry3Aa1  | : | ELSG-----  | NNLQIGWTGLSAGDKVYIDKIEFIPWN-----                       |                  | : | 652 |
| cry3Bb   | : | GFSGD----  | KNELIIGAESFVSNEKIYIDKIEFIPVQL-----                     |                  | : | 652 |
| cry4Aa   | : | KFAPN----  | QNISLVFNRSVYTNITVLIDKIEFLPITRSIREDRKQKLETVQQIINTFYAN   | :                |   | 703 |
| cry4Ba   | : | VPMLSSNQLITIAIQPLNMTSNNQVIIDRIEIIPIITOSVLDETENQNLESEREVVNALFTN | :  |                  |   | 659 |
| cry6Aa   | : | -----  | -----  | :                |   | -   |
| cry7Aa   | : | QFPDE----  | HPKITLHLSDLNNSFFVDSIEFIPVDVNYAEK----                   | EKLEKAQKAVNTLFTE | : | 659 |
| cry8Aa   | : | QFRET----  | QDKILLSMGDFSSGQEVYIDRIEFIPVDETYEAE---                  | QDLEAAKKAVALFTN  | : | 684 |
| cry10Aa  | : | PNKTPEG-EDTLMTLYGTPNHSYNIYIDKIEFIPITQSVLDYTEKQNIKTQKIWNDFVN    | :  |                  |   | 675 |
| cry16Aa  | : | DLTME-----   | VITYPYGRQFVEDIPSLILDKIEFLPTN-----                      |                  | : | 648 |
| cry19Ba  | : | SGGPS-----   | ISSNTLWLDNFSNGPVIIDKIEFIPGLITLNQAQGYDTYDQNAANGMYHQNYS  | :                |   | 663 |
| cry24Aa  | : | PEENN-----   | FAFTIDLESGGDLFIDKIEFIPVSGSAFEYEGKQNIKTQKAVNDLFIN       | :                |   | 674 |
| cry25Aa  | : | YFDSAP-----  | RIRLLRQPG-RLLVDRIEIIPWNFFPLSE-----                     | QENKSVDSLFIN     | : | 675 |
| cry39Aa1 | : | RASVAG-----  | YTNFTIEAGFGPPVYIDKIEFIPDNITTTILEYEGGRDLEKTKNAVNDLFTN   | :                |   | 659 |
| cry40Aa1 | : | -----  | GVEIIIQNLDTPINVDKVEFIPVNSTALEYEGKQSLKQAQDVVNDLFVK      | :                |   | 666 |

|              |   |  |                                      |    |    |    |   |    |   |     |
|--------------|---|--|--------------------------------------|----|----|----|---|----|---|-----|
|              | * | 20   | *                                    | 40 | *  | 60 | * | 80 | * | 100 |
| axmi008-orf2 | : | VSPMFTSSTKNTLKIEITDYEIDQAAISTECMSDEQNPOEKINLWDEIKLAKQLSQSRNLLQN----  | GFSGNDUTTFGNDIILIGSNNPIFKCKFLQMRGAR  | :  | 97 |    |   |    |   |     |
| cry19Aa-orf2 | : | VNFMLTSGAKNNLKLKLETTDYEIDQMANAIEHNSGEQYSQEKMMQWHDIKYAKQLSQARNLLQNG-- | FEDLFSGUTTSNQMSIQADNATFKENYLHMSGAR   | :  | 99 |    |   |    |   |     |
| crybun2orf2  | : | ---MFTSNIKNTLKIEITDYEIDQAAISTECMSNEHSKEEMMLWDEVQAKQLSWSRNLLYNG--     | FEDVSNCGKTSNTIEIRENSPVFKGHYLMFGAR    | :  | 96 |    |   |    |   |     |
| crybun3orf2  | : | ---MFTMGTKNTLKIEITDYEIDQAAISTECMSDEHSPKEMMLWDEVKRAKLISQSRNLLQNG      | FDFGYGNDWKFGNNIILIGSNNPIFKCNFLQMSGAR | :  | 97 |    |   |    |   |     |
| cry4Aa       | : | INTFYANPIKNTLQSELTDYDIDQAAANLVECTISEELYPKEMMLLDEVKNAKLISQSRNVLQNG--  | DFESATLGTWTTSDNITIQEDDPIFKGHYLMMSGAR | :  | 99 |    |   |    |   |     |
| cry4Ba       | : | VNALFTNDAKDALNIGTTDYDIDQAAANLVECTISEELYPKEMMLLDEVKNAKLISQSRNVLQNG--  | DFESATLGTWTTSDNITIQEDDPIFKGHYLMMSGAR | :  | 99 |    |   |    |   |     |

  

|              |   |  |  |     |     |     |   |     |   |     |
|--------------|---|--|--|-----|-----|-----|---|-----|---|-----|
|              | * | 120  | *  | 140 | *   | 160 | * | 180 | * | 200 |
| axmi008-orf2 | : | DIYGTLPPTYICQKIDESKLIKPYTRYRVRGFWGSSKOLKLMVTRYGKEIDAIMNVPMDLAYMQPNPSCGYRCESS---- | SQYVWSQGYPTP--TDGYAPDM                   | :   | 192 |     |   |     |   |     |
| cry19Aa-orf2 | : | DIYGTLPPTYIYQKIDESKLIKPYTRYLVRGFWGSSKOLELWVRVYGKEIDTVMNVPMNDIPYVP                | SMPVPCNELYDGGQQPYPMNRHVGYNPMVPVSQPSYTSDT | :   | 199 |     |   |     |   |     |
| crybun2orf2  | : | DIDGTLFPPTYIYQKIEESKLIKPYTRYRVRGFWGSSKOLKLMVTRYGKEIDAMNVPMNDLAYMQ                | PTPSCGDSRCESS----SRVWSQGYPTPV--TDGYASGR  | :   | 192 |     |   |     |   |     |
| crybun3orf2  | : | DIYGTLPPTYIYQKIDESKLIKPYTRYRVRGFWGSSKOLRLMVTRYGKEIDAMNVPMNDLAYMQ                 | PNPSCGDSRCESS----SQYVWSQGYPTP--TDGYAPDR  | :   | 192 |     |   |     |   |     |
| cry4Aa       | : | DIDGTLFPPTYIFQKIDESKLIKPYTRYLVRGFWGSSKOVELVVSRYGEEIDAIMNVPADLNLYLP----           | STFDCEGS-----NRCETSAVPANIGNTSDML         | :   | 190 |     |   |     |   |     |
| cry4Ba       | : | DIDGTLFPPTYIFQKIDESKLIKPYTRYLVRGFWGSSKOVELVVSRYGEEIDAIMNVPADLNLYLP----           | STFDCEGS-----NRCETSAVPANIGNTSDML         | :   | 190 |     |   |     |   |     |

  

|              |   |  |   |     |     |     |   |     |   |     |
|--------------|---|--|---|-----|-----|-----|---|-----|---|-----|
|              | * | 220  | *   | 240 | *   | 260 | * | 280 | * | 300 |
| axmi008-orf2 | : | YACQONIDRKHKVCHDRHPFD  | FHIDTTEVDVTNINVGDVLLKISNPDGYATVGNLEVIEEGPLTCEALAHVKQKEKKQKHMEKKRWETQOAYDPAKQAV  | :   | 292 |     |   |     |   |     |
| cry19Aa-orf2 | : | CQCTP--GKKHVCHDSHQFKFHIDTTEVDVYNINLGIVLFKISSPDGYATLDNLEVIEEGPVRC | EAVTHVKQKEKKQNHQMEKKRMEIKRVVDRAKQAV   | :   | 297 |     |   |     |   |     |
| crybun2orf2  | : | YACQSWRGTKHKVCHDRHPFD  | FHIDTTEELDTNINVGDVLFKISNPDGYATLGNLEVIEEGPLTCEALTHVKQKEKKQKHMEKKRWETQOAYDPAKQAV  | :   | 292 |     |   |     |   |     |
| crybun3orf2  | : | YACPSSSDKKHVMCHDRHPFD  | FHIDTTEELDTNINVGDVLFKISNPDGYATLGNLEVIEEGPLTCEALTHVKQKEKKQKHMEKKRWETQOAYDPAKQAV  | :   | 292 |     |   |     |   |     |
| cry4Aa       | : | YSCQYDTCGKKHVVCQDSHQFST  | IDTTEALDTMENIGVGVVMFKISSPDGYASLDNLEVIEEGPIDGEALSRVKHMEKKQNDQNEAKRSETQOAYDPAKQAI | :   | 290 |     |   |     |   |     |
| cry4Ba       | : | YSCQYDTCGKKHVVCQDSHQFST  | IDTTEALDTMENIGVGVVMFKISSPDGYASLDNLEVIEEGPIDGEALSRVKHMEKKQNDQNEAKRSETQOAYDPAKQAI | :   | 290 |     |   |     |   |     |

FIG. 2A

|              |   |                    |         |     |     |     |     |     |     |     |     |
|--------------|---|--------------------|---------|-----|-----|-----|-----|-----|-----|-----|-----|
| exmi008-orf2 | : | DALFTNE--QELHYHITL | 320     | *   | 340 | *   | 360 | *   | 380 | *   | 400 |
| cry19Aa-orf2 | : | DALFTG----         | EELNYDV | 320 | *   | 340 | *   | 360 | *   | 380 | *   |
| crybun2orf2  | : | DALFTNE--QELHYHITL | 320     | *   | 340 | *   | 360 | *   | 380 | *   | 400 |
| crybun3orf2  | : | DTLFTNE--QELHYHITL | 320     | *   | 340 | *   | 360 | *   | 380 | *   | 400 |
| cry4Aa       | : | DALFTNVQDEALQ      | 320     | *   | 340 | *   | 360 | *   | 380 | *   | 400 |
| cry4Ba       | : | DALFTNVQDEALQ      | 320     | *   | 340 | *   | 360 | *   | 380 | *   | 400 |
| exmi008-orf2 | : | LSNWSAGVSNLHAQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| cry19Aa-orf2 | : | LSNWSAGVSNLHVQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| crybun2orf2  | : | LSNWSAGVSNLHVQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| crybun3orf2  | : | LSNWSAGVSNVHLQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| cry4Aa       | : | LSNWSAGVSNVHLQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| cry4Ba       | : | LSNWSAGVSNVHLQ     | 420     | *   | 440 | *   | 460 | *   | 480 | *   | 500 |
| exmi008-orf2 | : | LHTGMYEQSYNGN      | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |
| cry19Aa-orf2 | : | QNMNMYDQSYSGN      | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |
| crybun2orf2  | : | PHTGMYCQSYNGN      | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |
| crybun3orf2  | : | PHTGMYCQSYNGN      | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |
| cry4Aa       | : | -----              | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |
| cry4Ba       | : | -----              | 520     | *   | 540 | *   | 560 | *   | 580 | *   | 600 |

FIG. 2B